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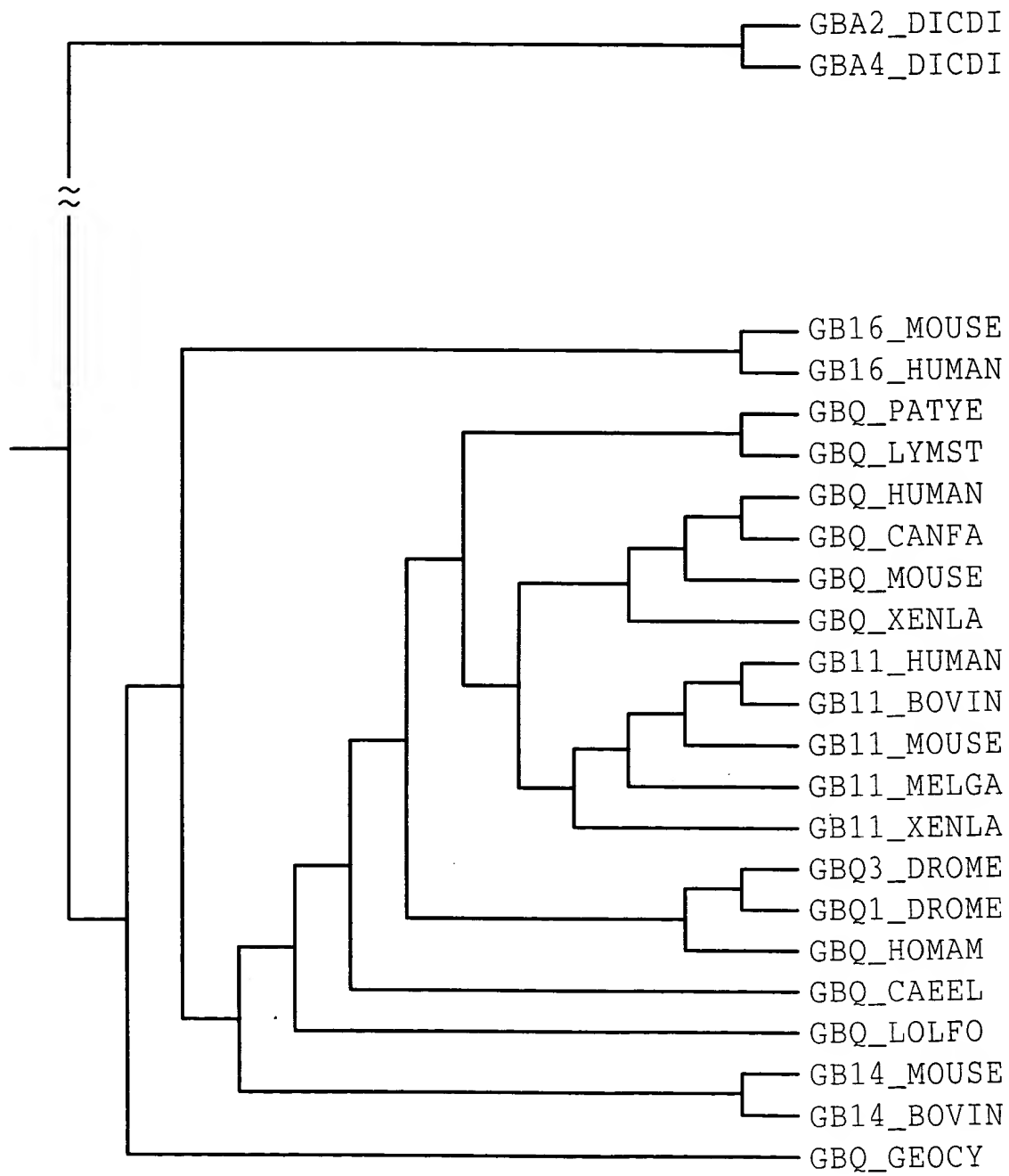


FIGURE 2A

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*C. elegans*  $G\alpha_{q/25}$ 

1 MACCLSEEAR EQKRINQEIE KQLQORDKRNA RRELKLLLLG TGESGKSTFI KQMRIIHGQG  
 61 YSEEDKRAHI RLVIQNVFMA IQSMIRAMDT LDIKFGNESE ELQEKAHVVR EVDFESVTSF  
 121 EEPYVSYIKE LWEDSGIQEC YDRRREYQLT DSAKYLLSDL RRLAVPDYLP TEQDILRVRV  
 181 PTTGIIEYPF DLEQIIFRMV DVGGQRSERR KWIHCFENVT SIMFLVASE YDQVLVECDN  
 241 ENRMEESKAL FRTIITYPWF TNSSVILFLN KKDLEEKIL YSHLADYFPE YDGPFRDPIA  
 301 AREFILKMFV DLNPDADKII YSHFTCATDT ENIRFVFAAV KDTILQHNLK **YIGLC**

*C. elegans*  $G\alpha_{q/29}$ 

1 MACCLSEEAR EQKRINQEIE KQLQORDKRNA RRELKLLLLG TGESGKSTFI KQMRIIHGQG  
 61 YSEEDKRAHI RLVIQNVFMA IQSMIRAMDT LDIKFGNESE ELQEKAHVVR EVDFESVTSF  
 121 EEPYVSYIKE LWEDSGIQEC YDRRREYQLT DSAKYLLSDL RRLAVPDYLP TEQDILRVRV  
 181 PTTGIIEYPF DLEQIIFRMV DVGGQRSERR KWIHCFENVT SIMFLVASE YDQVLVECDN  
 241 ENRMEESKAL FRTIITYPWF TNSSVILFLN KKDLEEKIL YSHLADYFPE YDGPFRDPIA  
 301 AREFILKMFV DLNPDADKII YSHFTCATDT ENIRFVFAAV KDTILQNNLK **YIGLC**

*C. elegans*  $G\alpha_{q/s9}$ 

1 MACCLSEEAR EQKRINQEIE KQLQORDKRNA RRELKLLLLG TGESGKSTFI KQMRIIHGQG  
 61 YSEEDKRAHI RLVIQNVFMA IQSMIRAMDT LDIKFGNESE ELQEKAHVVR EVDFESVTSF  
 121 EEPYVSYIKE LWEDSGIQEC YDRRREYQLT DSAKYLLSDL RRLAVPDYLP TEQDILRVRV  
 181 PTTGIIEYPF DLEQIIFRMV DVGGQRSERR KWIHCFENVT SIMFLVASE YDQVLVECDN  
 241 ENRMEESKAL FRTIITYPWF TNSSVILFLN KKDLEEKIL YSHLADYFPE YDGPFRDPIA  
 301 AREFILKMFV DLNPDADKII YSHFTCATDT ENIRFVFAAV KDTILQMHLR **QYELL**

*C. elegans*  $G\alpha_{q/s21}$ 

1 MACCLSEEAR EQKRINQEIE KQLQORDKRNA RRELKLLLLG TGESGKSTFI KQMRIIHGQG  
 61 YSEEDKRAHI RLVIQNVFMA IQSMIRAMDT LDIKFGNESE ELQEKAHVVR EVDFESVTSF  
 121 EEPYVSYIKE LWEDSGIQEC YDRRREYQLT DSAKYLLSDL RRLAVPDYLP TEQDILRVRV  
 181 PTTGIIEYPF DLEQIIFRMV DVGGQRSERR KWIHCFENVT SIMFLVASE YDQVLVECDN  
 241 ENRMEESKAL FRTIITYPWF TNSSVILFLN KKDLEEKIL YSHLADYFPE YDGPFRDPIA  
 301 AREFILKMFV DLNPDADKII YSHFTCATDT ENIRRVFND **RDIIQRMHLR QYELL**

*C. elegans*  $G\alpha_{q/i3(5)}$ 

1 MACCLSEEAR EQKRINQEIE KQLQORDKRNA RRELKLLLLG TGESGKSTFI KQMRIIHGQG  
 61 YSEEDKRAHI RLVIQNVFMA IQSMIRAMDT LDIKFGNESE ELQEKAHVVR EVDFESVTSF  
 121 EEPYVSYIKE LWEDSGIQEC YDRRREYQLT DSAKYLLSDL RRLAVPDYLP TEQDILRVRV  
 181 PTTGIIEYPF DLEQIIFRMV DVGGQRSERR KWIHCFENVT SIMFLVASE YDQVLVECDN  
 241 ENRMEESKAL FRTIITYPWF TNSSVILFLN KKDLEEKIL YSHLADYFPE YDGPFRDPIA  
 301 AREFILKMFV DLNPDADKII YSHFTCATDT ENIRFVFAAV KDTILQHNLK **ECGLY**

FIGURE 2B

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*D. melanogaster*  $G\alpha_{q/z5}$

1	MECCLSEEA	EQRINQIE	KQLRRDKRDA	RRELKLLLLG	TGESGKSTFI	KQMRIIHGSG
61	YSDDEKRGYI	KLVFQNI	FMA MQSMIKAMDM	LKISYGQGEH	SELADLVMSI	DYETVTTTFED
121	PYLNAIKTLW	DDAGIQECYD	RRREYQLTDS	AKYYLKDLDR	VAQPAYLPTE	QDILRVRVPT
181	TGIIEYPFDL	EEIRFRMVDV	GGQSRERRKW	IHCFENVTSI	IFLVALSEYD	QILFESDNEN
241	RMEESKALFR	TIITYPWFQN	SSVILFLNKK	DLLEEKIMYS	HLVDYFPEYD	GPQRDAITAR
301	EFILRMFVDL	NPDSEKIIYS	HFTCATDTEN	IRFVFAAVKD	TILQSNLKYI	<b>GLC</b>

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FIGURE 3

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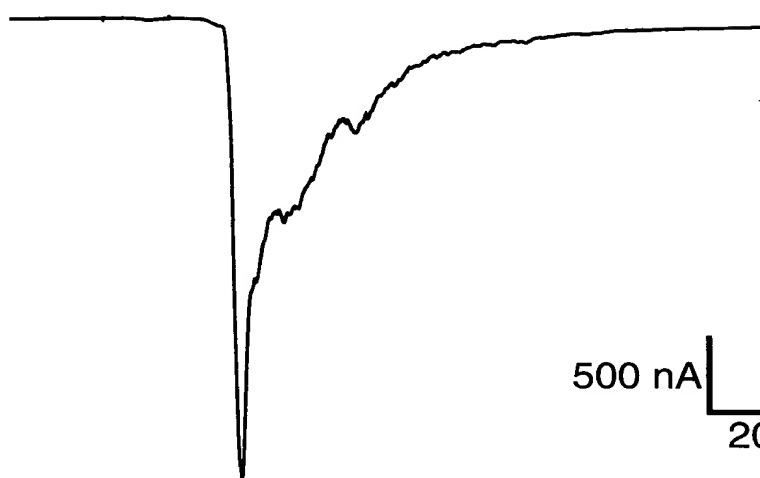
hNPFF1

NPFF 1 $\mu$ M



hNPFF1 + cG $\alpha_{q/z5}$

NPFF 1 $\mu$ M



hNPFF1 + cG $\alpha_{q/z5}$   
+ 190 ng EGTA

NPFF 1 $\mu$ M



FIGURE 4

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# Human D1

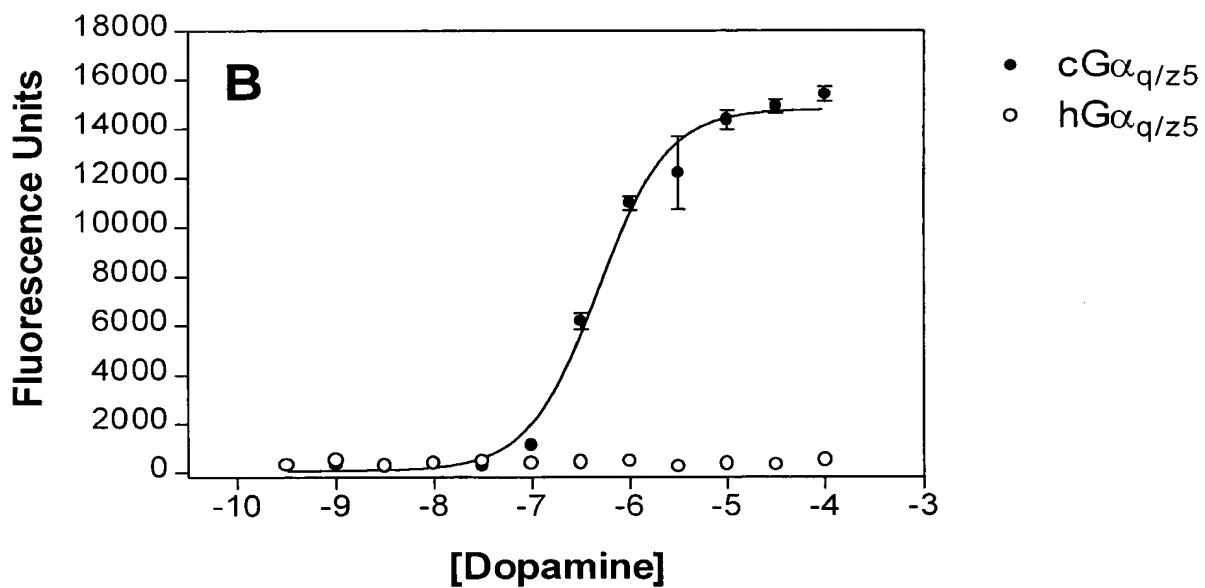
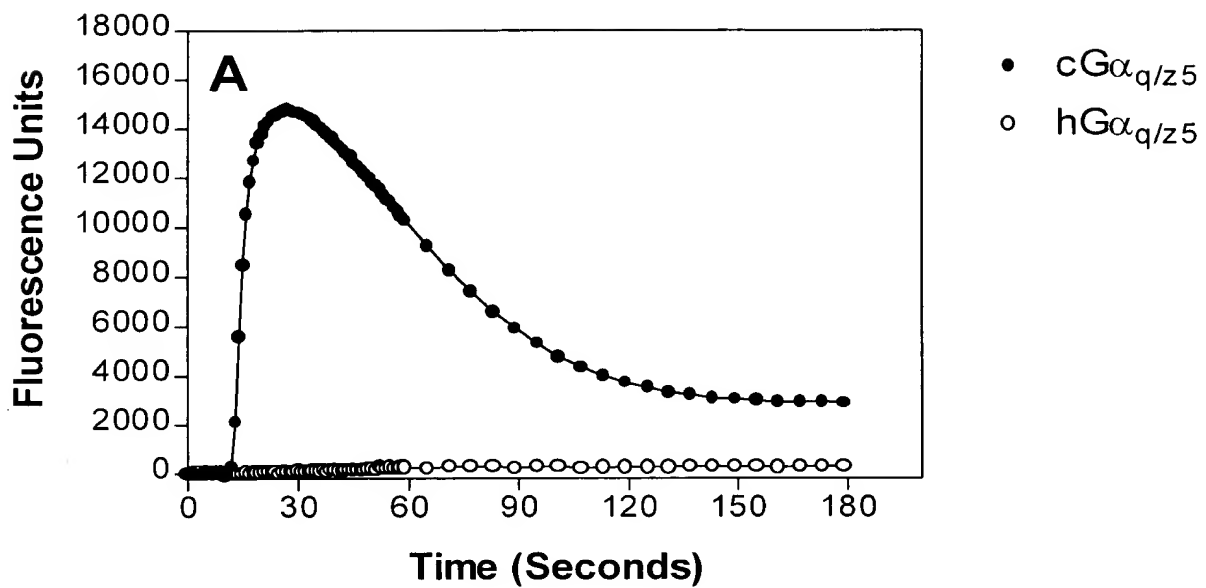


FIGURE 5A

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      *           20           *           40           *
GBQ_HUMAN : MTLESIMACCLSEFAKEARRINDEIERQLRRDKRDARREIKLLLLLGTGES
GBQ_CANFA  : MTLESIMACCLSEFAKEARRINDEIERQLRRDKRDARREIKLLLLLGTGES
GBQ_MOUSE  : MTLESIMACCLSEFAKEARRINDEIERHVRDKRDARREIKLLLLLGTGES
GBQ_XENLA  : MTLESIMACCLSEFAKEARRINDEIERQLRRDKRDARREIKLLLLLGTGES
GBQ_PATYE  : ~~~~~MACCLSEFAKEQKRINCEIEKELRKAKRDARREIKLLLLLGTGES
GBQ_LYMST  : ~~~~~MACCIPDELKEQKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ1_DROM  : ~~~~~MEGCLSEFAKEQKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ3_DROM  : ~~~~~MEGCLSEFAKEQKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_HOMAM  : ~~~~~MACCLSEFAKEQKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_LIMPO  : ~~~~~MACCLSEEGKEQKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_LOLFO  : ~~~~~MACCLSEFAKEQKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_CAEL   : ~~~~~MACCLSEFAKEQKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_GEOCY  : ~~~~~MSGLSEERLQKRINTRINREIQRDCHKDAKKEIKLLLLLGTGES

      60           *           80           *           100
GBQ_HUMAN  : GKSTFIKQMRIIHGSGYSDEDKRGFTKLIVYONIFETAMQAMIRAMDTLKTP
GBQ_CANFA  : GKSTFIKQMRIIHGSGYSDEDKRGFTKLIVYONIFETAMQAMIRAMDTLKTP
GBQ_MOUSE  : GKSTFIKQMRIIHGSGYSDEDKRGFTKLIVYONIFETAMQAMIRAMDTLKTP
GBQ_XENLA  : GKSTFIKQMRIIHGSGYSDEDKRGFTKLIVYONIFETAMQAMIRAMDTLKTP
GBQ_PATYE  : GKSTFIKQMRIIHGTGYSEEDKRGFTKLIVYONIFETAMHSMIRAMDTLKTP
GBQ_LYMST  : GKSTFIKQMRIIHGAGYSDEDKRSHIKIVYONIFETAMHAMIRAMDTLKTP
GBQ1_DROM  : GKSTFIKQMRIIHGSGYSDEDKRGYIKLVFONIFETAMQSMIKAMDMLKTP
GBQ3_DROM  : GKSTFIKQMRIIHGSGYSDEDKRGYIKLVFONIFETAMQSMIKAMDMLKTP
GBQ_HOMAM  : GKSTFIKQMRIIHGAGYSDEDKRGYIKLVFONIFETAMQSMIRAMDLLKTP
GBQ_LIMPO  : GKSTFIKQMRIIHGQGYSDDKSYIKLVYONIFETAMQSMNKAMEMKTP
GBQ_LOLFO  : GKSTFIKQMRIIHGSGYSEEDKRGFEKIVYONIFETAIQTLIAAMETLSLE
GBQ_CAEL   : GKSTFIKQMRIIHGQGYSEEDKRAHRLVYONVEMAIQSMIRAMDTLKTP
GBQ_GEOCY  : GKSTFIKQMRIIHCKGYSKQCLEYKNLMFRNIIILMSMHSMLQATAEKTP

      *           120           *           140           *
GBQ_HUMAN  : YKYEHNK--AHAQLVREVDVEKVS----AFENPYVDAIKSLWNDPGIQEC
GBQ_CANFA  : YKYEHNK--AHAQLVREVDVEKVS----AFENPYVDAIKSLWNDPGIQEC
GBQ_MOUSE  : YKYEHNK--AHAQLVREVDVEKVS----AFENPYVDAIKSLWNDPGIQEC
GBQ_XENLA  : YKYEHNK--GHALLVREVDVEKVA----SFENPYVDAIKSLWNDPGIQEC
GBQ_PATYE  : FEVADNE--ENAIMIRQVDYETVT----TLDSQSVEATLSLWADAGIQEC
GBQ_LYMST  : YINPANR--ENGNMIRQVDYETVT----TEDKPCVDAIKSLWNDPGIQEC
GBQ1_DROM  : YGQGEHS--ELADLVMSIDYETVT----TEDPYLNAIKTLWDDAGIQEC
GBQ3_DROM  : YGQGEHS--ELADLVMSIDYETVT----TEDPYLNAIKTLWDDAGIQEC
GBQ_HOMAM  : VGDSANI--EHADLVRSVDYESVT----TEEPYVTAMNSLWQDTGQHC
GBQ_LIMPO  : YKDRNNI--ENAEVLVSVDYETVT----TEDSPYVEATIKSLWVDPGIQEC
GBQ_LOLFO  : YKDPSN--NEHAFLNSIDADSAD----IEEDGHVTAIKGCWTDPGMQEC
GBQ_CAEL   : FGNESEELQEKAAVVREVDVESVT----SEEPYVSYIKELWEDSGIQEC
GBQ_GEOCY  : YIDPD--AQRHVQLLMALRPETAQ----SLGGETCEATIKSLWQDAGVQEC

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FIGURE 5B

160 \* 180 \* 200

GBQ\_HUMAN : YDRRREYQ-LSDSTKYYLNDLDRVADPAYLEPTQODVLRVRVPTTGITIEYP  
 GBQ\_CANFA : YDRRREYQ-LSDSTKYYLNDLDRVADPAYLEPTQODVLRVRVPTTGITIEYP  
 GBQ\_MOUSE : YDRRREYQ-LSDSTKYYLNDLDRVADPSYLEPTQODVLRVRVPTTGITIEYP  
 GBQ\_XENLA : YDRRREYQ-LSDSTKYYLNDLDRIATHGYLEPTQODVLRVRVPTTGITIEYP  
 GBQ\_PATYE : YDRRREYQ-LTDSAKYYLDAVDRIAEPNYLEPTLODILRVRVPTTGITIEYP  
 GBQ\_LYMST : YDRRREYQ-LTDSAKYYLDSVERISQQDYLEPTLODILRVRVPTTGITIEYP  
 GBQ1\_DROM : YDRRREYQ-LTDSAKYYLSDLARIEQADYLEPTEQDILRVRVPTTGITIEYP  
 GBQ3\_DROM : YDRRREYQ-LTDSAKYYLKDLDRVAQPAYLEPTEQDILRVRVPTTGITIEYP  
 GBQ\_HOMAM : YDRRREYQ-LTDSAKYYLTDLRIAADKYVSTLODILRVRVPTTGITIEYP  
 GBQ\_LIMPO : YDRRREYQ-LTDSAKYYLNDIDRIAVPNYLEPTQODILRVRVPTTGITIEYP  
 GBQ\_LOLFO : YDRRREYQ-LTDSAKYYLDDVERIHEPGYIPTLODILRVRVPTTGITIEYP  
 GBQ\_CAEEL : YDRRREYQ-LTDSAKYYLSDLRRLAVPDYLEPTEQDILRVRVPTTGITIEYP  
 GBQ\_GEOCY : YDRRREYQ-LSDSTKYYLDDLPRISSNDYVPTTQODVLRVRVPTTGITIEYP

\* 220 \* 240 \*

GBQ\_HUMAN : FDLQSVIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_CANFA : FDLQSVIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_MOUSE : FDLQSVIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_XENLA : FDLQSVIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_PATYE : FDLDSIIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_LYMST : FDLDSIIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ1\_DROM : FDLDGIVIFFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ3\_DROM : FDLLEIRIFFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ\_HOMAM : FDLLEIRIFFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ\_LIMPO : FILDSTIIFFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ\_LOLFO : FDLYSIIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_CAEEL : FDLQSVIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_GEOCY : FTINKIIFFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOILVESD

260 \* 280 \* 300

GBQ\_HUMAN : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_CANFA : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_MOUSE : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_XENLA : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_PATYE : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMHSHLVDYF  
 GBQ\_LYMST : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMHSHLVDYF  
 GBQ1\_DROM : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ3\_DROM : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_HOMAM : N-ENRMEESKALFKTITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_LIMPO : N-ENRMEESKALFKTITTYPWFONSSVILFLNKKDLLEEKIMFSLHVDYF  
 GBQ\_LOLFO : NEENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMTSHLVDYF  
 GBQ\_CAEEL : N-ENRMEESKALFRITITTYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_GEOCY : SRVNRMVESLHLFNTITTSYPWENKSSIILFLNKKDLLEEKIMHSHLVDYF

FIGURE 5C

GBQ\_HUMAN : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKIIYSHETCATDTENIRFVFA  
 GBQ\_CANFA : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKIIYSHETCATDTENIRFVFA  
 GBQ\_MOUSE : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKIIYSHETCATDTENIRFVFA  
 GBQ\_XENLA : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKIIYSHETCATDTENIRFVFA  
 GBQ\_PATYE : PEFDGQKKDAQCAREFTLRMEVDLNPDPDKIIYSHETCATDTENIRFVFA  
 GBQ\_LYMST : PEFDGPKKEASTAREFTLRMEVELNPDPDKIIYSHETCATDTENIRFVFA  
 GBQ1\_DROM : PEYDGPQRDAITAREFTLRMEVDLNPDSKIIYSHETCATDTENIRFVFA  
 GBQ3\_DROM : PEYDGPQRDAITAREFTLRMEVDLNPDSKIIYSHETCATDTENIRFVFA  
 GBQ\_HOMAM : PEYDGPQRDAITAREFTLRMEVELNPDPDKIIYSHETCATDTENIRFVFA  
 GBQ\_LIMPO : PEYDGPKKDAVOGREFLLKMFVDLNPDSKIIYSHETCATDTENIRFVFA  
 GBQ\_LOLFO : PDYDGPKCDEYEAAREFMDSYMDLNECKEKMYYHYTCATDTENIRFVFA  
 GBQ\_CAEEL : PEYDGPQRDPIAAREFTLRMEVDLNPDPADKIIYSHETCATDTENIRFVFA  
 GBQ\_GEOCY : EEYDGPKCDEHVSARESTAKMESISINDMRSADTYPHETCATDTENIKEVFD

GBQ\_HUMAN : AVKDTIILQLNLKEYNAV~~~ : 359  
 GBQ\_CANFA : AVKDTIILQLNLKEYNLV~~~ : 359  
 GBQ\_MOUSE : AVKDTIILQLNLKEYNLV~~~ : 359  
 GBQ\_XENLA : AVKDTIILQLNLKEYNLV~~~ : 359  
 GBQ\_PATYE : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ\_LYMST : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ1\_DROM : AVKDTIIMONALKEFNLC~~~ : 353  
 GBQ3\_DROM : AVKDTIILQSNLKEYNLV~~~ : 353  
 GBQ\_HOMAM : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ\_LIMPO : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ\_LOLFO : AVKDTIILQLNLKEYNLV~~~ : 354  
 GBQ\_CAEEL : AVKDTIILQHNLEKEYNLV~~~ : 355  
 GBQ\_GEOCY : VVKNHILQQHITF--VWPGL : 355